



REPLACEMENT SHEET

RLE/RLE MOTIF

CaCAP1 1 MSTESQFNVQGYNIITILKRLAEATSRLEDITIFQEEANKNHYGVDLSLTKETGPKSRTVESSEATSDGKSLESTSFATFSEAPV 85
ScCAP1 1 MPDSKYTMQGYNLVKLLKRLAEATARLEDVTIYQEGYQNKLEAS---KNNKP-----SDSGADANTNEPSAENAPEVEQ 73
SpCAP1 1 MSDMINIRETGYNFTTILKRLAEATSRLEDLVESGHKPLPNMHRPSR-DSNSQTHNISFNIGTPTAPTIVTSGSPAVASLHDQVA 83
MouseCAP1 1 MADMQNLVERLERAVGRLEAVSHTSDMH-----CGYGDSPS-----K 37
HumanCAP1 1 MADMQNLVERLERAVGRLEAVSHTSDMH-----RGYADSPSK-----A 38

CaCAP1 86 EKS-----KLIVFENFVESYVHPLVETSKKIDSLVGESAQYFEAFVEQKFELEVLVLSQSQPDMTDPALAKA 153
ScCAP1 74 DP-----KCIATFQSYIGENIDPLVELSGKIDTVLDALQLLKGFGQSQTLFLRAAVRSRKPDPDYSSQTFADS 140
SpCAP1 84 AAISPRNRSLTSTSAVEAPASISAYDEFCSKYLKSKYMELSKKIGGLIAEQSEHVEKAFNLLRQVLSVALKAQKPDMDSPELLE 168
MouseCAP1 38 GAV-----PYVQAFDLSLLANPVAEYLKMSKEIGGDVQKHAEMVHTGLKLERALLATASQCQQP--AGNKLSDL 103
HumanCAP1 39 GAA-----PYVQAFDLSLLAGPVAEYLKISKEIGGDVQKHAEMVHTGLKLERALLVTSQCQQP--AENKLSDL 104

CaCAP1 154 LEPMNAKCTKINELKDSNRKSPFFNHLSTFSESNAVFYWIPIP-TPVSYITDTKDTVKFWSDRVLKEYKTKDQVHVVEWVKQTL 237
ScCAP1 141 LRPINENIILKGLKESNRQSKYFAYLSALSEGAPLFSWVAVD-TPVSMVTDFKDAAQFWTNRLKEYRESDENAVWVKFLAS 224
SpCAP1 169 LKPIQSELLTITNIRDEHRTAPEFNQLSTVMSGISILGWVTVETPLSFMSKMSQGFYANRVMKEFKGDDILQIEWVRSYLT 253
MouseCAP1 104 LAPISEQIQEVITFREKNRGSKFFNHL SAVSESIQALGWALAAKPGPFVKEMNDAAAMFYTNRVLKEYRDVDRKKHVDVVRAYLSI 188
HumanCAP1 105 LAPISEQIQEVITFREKNRGSKFFNHL SAVSESIQALGWAMAPKPGPYVKEMNDAAAMFYTNRVLKEYKVDKDKHVDVVKAYLSI 189

POLYPROLINE REGION

CaCAP1 238 FDELKNYVKEYHTTGVAWNPKGKPFPAEVVSQOTESAAKNSS--SASGSAGGAAPPPPPPPPPATFDDTEKDSNPSPAS-GGINA 320
ScCAP1 225 FDNLKAYIKEYHTTGVSWKKDGMDFADAMAQSTKNTGATSSPSPASATAAPAPPPPPPPAPPASVFEISNDTPATSSDANKGGIGA 309
SpCAP1 254 LTELITYVKTHTFKTGLTWSTKQDAVPLKTALANLSASKTQAPSSGDSANGGLPPPPPPPPPPPSNDFWKDSNEP-APADNK-GDMGA 336
MouseCAP1 189 WTELQAYIKEFHHTTGLAWSKTG-----PVAKELSLPSGSPSVGSGPPPPPPPPPPPIPTS-----SGSDDS-ASRSA 255
HumanCAP1 190 WTELQAYIKEFHHTTGLAWSKTG-----PVAKELSLPSGSPSAGSGPPPPPPPPPPPVSTST-----SGSDES-ASRSA 256

SH3 BINDING MOTIFS

CaCAP1 321 VFAELNQGANITSGLKKVKDKSEMTHKNPPELRKQPPVAPK--KPAPFKKPSLSGG-VSSAPVKKPAKKELIDGTKWIIQNFTKAD 402
ScCAP1 310 VFAELNQGANITGKLKKVKDKSQQTHKNPELRQSSTVSTGSKSGPPPRPK--KP-----STLKTKRPPRKELVG-NKWFIEYEN-- 386
SpCAP1 337 VFAEINKGEGITSGLRKKVKDKSEMTHKNPNLR-----KTGTPGPKPKIKSSAPSKPAETAAPVKPPRIELEN-TKWFEVENQVD-- 412
MouseCAP1 256 LFAQINQGESITHALKHVSDDMKTHKNPALKAQSGPVRSGPKPFSAPKPQ-TSPS-PKPATKKEPALLELEG-KKWRVENQEN-- 335
HumanCAP1 257 LFAQINQGESITHALKHVSDDMKTHKNPALKAQSGPVRSGPKPFSAPKPQ-TSPS-PKRATKKEPALLELEG-KKWRVENQEN-- 336

FIG. 3A

| | | | |
|-----------|-----|---|-----|
| CaCAP1 | 403 | ISDLSPITIEVEMHQSVFIGNCSDVTIQLKGKANAVSVSETKNVALVIDSLISGVDVIKSKFGIQVLGLVPMLSIDKSDEGTIY | 487 |
| ScCAP1 | 387 | --ETESLVIDANKDESIFIGKCSQVLVQIKGVNAISLSETESCSVLDSSISGMDVIKSNKFGIQVNHSLPQISIDKSDGGNIY | 469 |
| SpCAP1 | 413 | --NHSIVLDSVELNHSVQIFGCSNCTIILKGLINTVSMCNCKRTSVVVDTLVAAFDAKCSNFGCQVMNHVPMIVIDQCDGGSIIY | 495 |
| MouseCAP1 | 336 | --VSNLVIDDTELKQVAYIYKCVNTTLQIKGKINSITVDNCKKGLGVFDDVVGIVEIINSRDVKVQVMGKVPTISINKTDGCHAY | 418 |
| HumanCAP1 | 337 | --VSNLVIEDTELKQVAYIYKCVNTTLQIKGKINSITVDNCKKGLGVFDDVVGIVEIINSKDVKVQVMGKVPTISINKTDGCHAY | 419 |
| CaCAP1 | 488 | LSQESIDNDSQVFTSSTTALNINAPK-ENDDYEELAVPEQFVSKVNVN-GKLVTTQIVEHAG | 545 |
| ScCAP1 | 470 | LSKESLN--TEIYTSCTAINVNLPIGEDDDYVEFPIPEQMKSFSAD-GKFSAVFEHAG | 526 |
| SpCAP1 | 496 | LSKSSLS--SEVVTSKSTSLNINVPN-EEGDYAERAVPEQIKHKVNEKGELVSEIVRHE | 551 |
| MouseCAP1 | 419 | LSKNSLD--CEIVSAKSSEMNVLIPT-EGGDFNEFPVPEQFKTLWNG-QKLVTTTTEIAG | 474 |
| HumanCAP1 | 420 | LSKNSLD--CEIVSAKSSEMNVLIPT-EGGDFNEFPVPEQFKTLWNG-QKLVTTTTEIAG | 475 |

FIG. 3B

REPLACEMENT SHEET

| | | | |
|----------|-----|---|-----|
| CaPDE2 | 335 | NPIQTLGLLVAALGHDVGHPGTNDFMIFSAPTALLY | 372 |
| ScPDE2 | 288 | NPVQTLLLCMAAIGHDVGHPGTNNQLLCNCESEVAQNF | 325 |
| HuPDE2A3 | 682 | EDIEIFALFISCMCHDLDRGTNNSFQVASKSVLAALY | 719 |
| CaPDE2 | 373 | NDR-SVLESYHASLFINKVLRICWPDLLTCTIEEKSEL | 409 |
| ScPDE2 | 326 | KNV-SILENFHRELFQ-QLLSEHWP--LKLSISKKK-- | 357 |
| HuPDE2A3 | 720 | SSEGSMERHHFAQAI-AILNTHGCN-IFDHFSRKDYQ | 755 |
| CaPDE2 | 410 | TIRSLIISSILATDMGEHNEYVNRLLKSFKTHNEILNHD | 447 |
| ScPDE2 | 358 | --FDFISEAILATDMALHSQYEDRLMHENPMKQIT--- | 390 |
| HuPDE2A3 | 756 | RMLDLMRDIIILATDLAHLRIFKDLQKMAEVGYDRNNK | 793 |
| CaPDE2 | 448 | NTVKLIISALLIKCADISNVTRPLRVSAQWAMVLSREF | 484 |
| ScPDE2 | 391 | -----LISLIKAADISNVTRTLISARWAYLITLTF | 422 |
| HuPDE2A3 | 794 | QHHRLLLCLLMTSCDLSQTKGWKTTRKIAELIYKEF | 830 |

FIG. 13